

7% **(SEQ ID NO: 6)** (Gly)-(Asp)-(Thr)-(Pro)-(Thr)-(Leu)-(His)-(Glu)-.....
20% **(SEQ ID NO: 7)** (His)-(Gly)-(Asp)-(Thr)-(Pro)-(Thr)-(Leu)-(His)-.....

Please delete the paragraph on page 49, line 14 to line 20 and replace it with the following paragraph:

The interpretation of the obtained fragments on the basis of known sequence information allows the following conclusion.

fragment 1 (N-terminus): **(SEQ ID NO: 8)** (Met)-(His)-(Gly)-(Asp)-(Thr)-(Pro).....
fragment 2 (cleaved at AA 49): **(SEQ ID NO: 9)**(Ala)-(His)-(Tyr)-(Asn)-(Ile)-(Val).....
fragment 3 (cleaved at AA 60): **(SEQ ID NO: 10)** (Cys)-(Asp)-(Ser)-(Thr)-(Leu)-(Arg).....
fragment 4 (cleaved at AA 66): **(SEQ ID NO: 11)** (Leu)-(Cys)-(Val)-(Gln)-(Ser)-(Thr).....
fragment 5 (cleaved at AA 77): **(SEQ ID NO: 12)** (Thr)-(Leu)-(Glu)-(Asp)-(Leu)-(Leu).....

Please delete the paragraph on page 84, line 28 to page 85, line 16 and replace it with the following paragraph:

As confirmed by N-terminal sequencing, the main sequence is 100% in agreement with the expected N-terminal sequence of the E7 protein of human papilloma virus type 18. The main sequence was: (Met)-(His)-(Gly)-(Pro)-(Lys)-(Ala)-(Thr)-(Leu) **(SEQ ID NO: 13)**. One of the minor signals at each position was brought into agreement with the n-1 mer of the protein: (His)-(Gly)-(Pro)-(Lys)-(Ala)-(Thr)-(Leu)-(Gln) **(SEQ ID NO: 14)**; this was approx. 16 - 20% with regard to the main sequence. The remaining minor signals were brought into agreement with the n-12 mer of the protein: (His)-(Leu)-(Glu)-(Pro)-(Gln)-(Asn)-(Glu)-(Ile) **(SEQ ID NO: 15)**; this again was approx. 16 - 20% with regard to the main sequence. To conclude, 60 - 68% of the sample are full length HPV18-E7, 16 - 20 % are degraded at the N-terminus missing one amino acid (Met) and 16 - 20% are degraded at the N-terminus missing 13 amino acids (Met, His, Gly, Asp, Thr, Pro, Thr, Leu, Gln, Asp, Ile, Val, Leu). The

truncated protein has a calculated WM of 10.6 kDa compared to 12.0 kDa of the full length protein. The difference in size is also seen in SDS-PAGE, Fig.3.

Sequencing yield and result was:

position: 1 5
60 - 68% **(SEQ ID NO: 13)**(Met)-(His)-(Gly)-(Pro)-(Lys)-(Ala)-(Thr)-(Leu)-
.....
16 - 20% **(SEQ ID NO: 14)** (His)-(Gly)-(Pro)-(Lys)-(Ala)-(Thr)-(Leu)-(Gln).....

position: 15 20
16 - 20% **(SEQ ID NO: 15)** (His)-(Leu)-(Glu)-(Pro)-(Gln)-(Asn)-(Glu)-(Ile).....

Please delete the paragraph on page 87, line 15 to line 24 and replace it with the following paragraph:

The interpretation of the obtained fragments on the basis of known sequence information allows the following conclusion: (* minor sequences)

fragment 1 (N-terminus): **(SEQ ID NO: 16)**(Met)-(His)-(Gly)-(Pro)-(Lys).....
fragment 2 (cleaved at AA 5): **(SEQ ID NO: 17)**(Ala)-(Thr)-(Leu)-(Gln)-(Asp)-(Ile).....
fragment 3* (N-terminus truncated): **(SEQ ID NO: 18)**(His)-(Leu)-(Glu)-(Pro)-(Gln)-(Asn).....
fragment 4 (cleaved at AA 52): **(SEQ ID NO: 19)**(Arg)-(Ala)-(Glu)-(Pro)-(Gln)-(Arg).....
fragment 5 (cleaved at AA 53): **(SEQ ID NO: 20)**(Ala)-(Glu)-(Pro)-(Gln)-(Arg)-(His).....
fragment 6* (cleaved at AA 58): **(SEQ ID NO: 21)**(His)-(Thr)-(Met)-(Leu)-(Cys)-(Met).....
fragment 7* (cleaved at AA 67): **(SEQ ID NO: 22)**(Cys)-(Glu)-(Ala)-(Arg)-(Ile)-(Glu).....
fragment 8* (cleaved at AA 71): **(SEQ ID NO: 23)** (Ala)-(Phe)-(Gln)-(Gln)-(Leu)-(Phe).....